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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/831,656

DATE: 09/27/2001

TIME: 11:59:29

Input Set : A:\5753prj.ST25.txt

Output Set: N:\CRF3\09272001\I831656.raw

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3 <110> APPLICANT: Novozymes A/S
 4 Nielsen, Jack Bech
 5 Kjaerulff, Soren
 7 <120> TITLE OF INVENTION: Transgenic Plant Expressing Maltogenic Alpha-Amylase
 9 <130> FILE REFERENCE: 5753.204-US
 11 <140> CURRENT APPLICATION NUMBER: 09/831,656
 C--> 12 <141> CURRENT FILING DATE: 2001-08-23
 14 <150> PRIOR APPLICATION NUMBER: PCT/DK99/00624
 15 <151> PRIOR FILING DATE: 1999-11-12
 17 <160> NUMBER OF SEQ ID NOS: 4
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 2160
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Bacillus sp.
 26 <400> SEQUENCE: 1

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31	ggggacgtga	tttaccagat	tatcattgac	cggttttacg	atggggacac	gacgaacaac	180
33	aatcctgccca	aaagttatgg	actttacgat	ccgaccaa	cgaaagtgga	aatgtattgg	240
35	ggcgggggatc	tggagggggt	tcgtcaaaaa	cttccttata	ttaaacagct	gggcgtaacg	300
37	acaatctggt	tgtccccggt	tttgacaat	ctggatacac	tggcgggcac	cgataaacag	360
39	ggctatcacg	gatactggac	gcgcgatttt	aaacagattg	aggaacattt	cgggaattgg	420
41	accacatttg	acacgttggt	caatgatgct	caccaaaccg	gaatcaaggt	gattgtcgac	480
43	tttgtgccca	atcattcgac	tccttttaag	gcaaacgatt	ccacctttgc	ggaaggcggc	540
45	gccctctaca	acaatggaac	ctatatgggc	aattattttg	atgacgcaac	aaaagggtag	600
47	ttccaccata	atggggacat	cagcaactgg	gacgaccggt	acgaggcgca	atggaaaaac	660
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55	aagaaagaca	ttttctggt	gggggaatgg	tacggagatg	accccggaac	agccaatcat	900
57	ctggaaaagg	tccggtacgc	caacaacagc	ggtgtcaatg	tgtctgattt	tgatctcaac	960
59	acggtgattc	gaaatgtgtt	cggcacattt	acgcaaacga	tgtacgatct	taacaatatg	1020
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65	gcttttcattc	tcacttcgcg	gggtacgccc	tccatctatt	atggaaccga	acaatacatg	1200
67	gcaggcgcca	atgaccgcta	caaccggggg	atgatgccgg	cgtttgatac	gacaaccacc	1260
69	gccttttaaag	aggtgtcaac	tctggcgggg	ttgcgcagga	acaatgcggc	gatccagtac	1320
71	ggcaccacca	cccagcgttg	gatcaacaat	gatgtttaca	tttatgaacg	gaaatttttc	1380
73	aacgatgtcg	tgttggtggc	catcaatcga	aacacgcaat	cctcctattc	gatttccggt	1440
75	ttgcagacgg	ccttgccaaa	tggcagctat	gcggattatc	tgtcagggct	gttggggggg	1500
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79	tctgtttggc	agtacagcac	atccgcttca	gcgccgcaaa	tcggatcggt	tgctccaaat	1620
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83	accgtgacat	ttggcggagt	gacagcgact	gtgaaatcct	ggacatccaa	tcggattgaa	1740
85	gtgtacgttc	ccaacatggc	cgccgggctg	accgatgtga	aagtcaccgc	gggtggagtt	1800
87	tccagcaatc	tgtattctta	caatattttg	agtggaaacgc	agacatcggt	tgtgtttact	1860

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91 gaattgggga attggagcac ggatacgagc ggagccgtta acaatgcgca agggcccctg 1980
93 ctgcgcgcca attatccgga ttggttttat gtattcagcg ttccagcagg aaagacgatt 2040
95 caattcaagt tcttcatcaa gcgtgcggat ggaacgattc aatgggagaa tggttcgaac 2100
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112 20 25 30
115 Ala Ser Ser Ser Ala Ser Val Lys Gly Asp Val Ile Tyr Gln Ile Ile
116 35 40 45
119 Ile Asp Arg Phe Tyr Asp Gly Asp Thr Thr Asn Asn Asn Pro Ala Lys
120 50 55 60
123 Ser Tyr Gly Leu Tyr Asp Pro Thr Lys Ser Lys Trp Lys Met Tyr Trp
124 65 70 75 80
127 Gly Gly Asp Leu Glu Gly Val Arg Gln Lys Leu Pro Tyr Leu Lys Gln
128 85 90 95
131 Leu Gly Val Thr Thr Ile Trp Leu Ser Pro Val Leu Asp Asn Leu Asp
132 100 105 110
135 Thr Leu Ala Gly Thr Asp Asn Thr Gly Tyr His Gly Tyr Trp Thr Arg
136 115 120 125
139 Asp Phe Lys Gln Ile Glu Glu His Phe Gly Asn Trp Thr Thr Phe Asp
140 130 135 140
143 Thr Leu Val Asn Asp Ala His Gln Asn Gly Ile Lys Val Ile Val Asp
144 145 150 155 160
147 Phe Val Pro Asn His Ser Thr Pro Phe Lys Ala Asn Asp Ser Thr Phe
148 165 170 175
151 Ala Glu Gly Gly Ala Leu Tyr Asn Asn Gly Thr Tyr Met Gly Asn Tyr
152 180 185 190
155 Phe Asp Asp Ala Thr Lys Gly Tyr Phe His His Asn Gly Asp Ile Ser
156 195 200 205
159 Asn Trp Asp Asp Arg Tyr Glu Ala Gln Trp Lys Asn Phe Thr Asp Pro
160 210 215 220
163 Ala Gly Phe Ser Leu Ala Asp Leu Ser Gln Glu Asn Gly Thr Ile Ala
164 225 230 235 240
167 Gln Tyr Leu Thr Asp Ala Ala Val Gln Leu Val Ala His Gly Ala Asp
168 245 250 255
171 Gly Leu Arg Ile Asp Ala Val Lys His Phe Asn Ser Gly Phe Ser Lys
172 260 265 270
175 Ser Leu Ala Asp Lys Leu Tyr Gln Lys Lys Asp Ile Phe Leu Val Gly
176 275 280 285
179 Glu Trp Tyr Gly Asp Asp Pro Gly Thr Ala Asn His Leu Glu Lys Val
180 290 295 300
183 Arg Tyr Ala Asn Asn Ser Gly Val Asn Val Leu Asp Phe Asp Leu Asn

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184 305          310          315          320
187 Thr Val Ile Arg Asn Val Phe Gly Thr Phe Thr Gln Thr Met Tyr Asp
188          325          330          335
191 Leu Asn Asn Met Val Asn Gln Thr Gly Asn Glu Tyr Lys Tyr Lys Glu
192          340          345          350
195 Asn Leu Ile Thr Phe Ile Asp Asn His Asp Met Ser Arg Phe Leu Ser
196          355          360          365
199 Val Asn Ser Asn Lys Ala Asn Leu His Gln Ala Leu Ala Phe Ile Leu
200          370          375          380
203 Thr Ser Arg Gly Thr Pro Ser Ile Tyr Tyr Gly Thr Glu Gln Tyr Met
204 385          390          395          400
207 Ala Gly Gly Asn Asp Pro Tyr Asn Arg Gly Met Met Pro Ala Phe Asp
208          405          410          415
211 Thr Thr Thr Thr Ala Phe Lys Glu Val Ser Thr Leu Ala Gly Leu Arg
212          420          425          430
215 Arg Asn Asn Ala Ala Ile Gln Tyr Gly Thr Thr Thr Gln Arg Trp Ile
216          435          440          445
219 Asn Asn Asp Val Tyr Ile Tyr Glu Arg Lys Phe Phe Asn Asp Val Val
220          450          455          460
223 Leu Val Ala Ile Asn Arg Asn Thr Gln Ser Ser Tyr Ser Ile Ser Gly
224 465          470          475          480
227 Leu Gln Thr Ala Leu Pro Asn Gly Ser Tyr Ala Asp Tyr Leu Ser Gly
228          485          490          495
231 Leu Leu Gly Gly Asn Gly Ile Ser Val Ser Asn Gly Ser Val Ala Ser
232          500          505          510
235 Phe Thr Leu Ala Pro Gly Ala Val Ser Val Trp Gln Tyr Ser Thr Ser
236          515          520          525
239 Ala Ser Ala Pro Gln Ile Gly Ser Val Ala Pro Asn Met Gly Ile Pro
240          530          535          540
243 Gly Asn Val Val Thr Ile Asp Gly Lys Gly Phe Gly Thr Thr Gln Gly
244 545          550          555          560
247 Thr Val Thr Phe Gly Gly Val Thr Ala Thr Val Lys Ser Trp Thr Ser
248          565          570          575
251 Asn Arg Ile Glu Val Tyr Val Pro Asn Met Ala Ala Gly Leu Thr Asp
252          580          585          590
255 Val Lys Val Thr Ala Gly Gly Val Ser Ser Asn Leu Tyr Ser Tyr Asn
256          595          600          605
259 Ile Leu Ser Gly Thr Gln Thr Ser Val Val Phe Thr Val Lys Ser Ala
260          610          615          620
263 Pro Pro Thr Asn Leu Gly Asp Lys Ile Tyr Leu Thr Gly Asn Ile Pro
264 625          630          635          640
267 Glu Leu Gly Asn Trp Ser Thr Asp Thr Ser Gly Ala Val Asn Asn Ala
268          645          650          655
271 Gln Gly Pro Leu Leu Ala Pro Asn Tyr Pro Asp Trp Phe Tyr Val Phe
272          660          665          670
275 Ser Val Pro Ala Gly Lys Thr Ile Gln Phe Lys Phe Phe Ile Lys Arg
276          675          680          685
279 Ala Asp Gly Thr Ile Gln Trp Glu Asn Gly Ser Asn His Val Ala Thr
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292 <220> FEATURE:
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301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <223> OTHER INFORMATION: RNP 110 ✓
307 <400> SEQUENCE: 4
308 cgatgagctc ctagttttgc cacgt 25

VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date